Conclusion: Demonstrating the association between the presence of oval cells and the progression of liver diseases could provide an useful marker for understanding the correlation between the presence of oval cells and progression of disease and creation of future treatment.

OL-006 Efficacy, tolerability and safety of personalized low-dose IFN treatment in patients with HCV-related liver cirrhosis and severe complications

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Object: To observe the efficacy, tolerability and safety of personalized low-dose IFN treatment in patients with HCV-related liver cirrhosis and severe complications.
Method: Personalized low-dose IFN treatment was performed in 61 patients. Less than 3 million units of personalized low-dose natural IFN-alpha was administered QOD intramuscularly or less than 50 μg Peg-IFN alpha-2b QW intrasubcutaneously, which depended on patients tolerability, and plus Ribavirin 600 mg/day. The course of treatment was at least 24 weeks. Some patients received more than 2 years IFN maintenance therapy.
Results: Twenty of the 62 patients showed a rapid virological response in 4 weeks treatment (32.25%). Twenty eight of 62 patients showed a complete early virological response in 12 weeks treatment (45.16%). Thirty four of 62 patients showed HCV RNA undetectable in 24 weeks IFN therapy (54.83%). ALT levels normalized (about 40 IU/L) at the end of 24 weeks therapy. 11 of 25 patients had a sustained virological response who were given more than 2 years Maintenance Therapy (44%). Definitive discontinuation of therapy was necessary in 7 patients (11.29 %) because of side effects.
Conclusion: Personalized low-dose IFN and ribavirin combination therapy was useful and safe in some patients with HCV-related liver cirrhosis and severe complications for whom standard-dose interferon and ribavirin combination therapy was difficult.

Free Paper Presentation 2 – Bacterial Infections/Antibiotics I

OL-007 Carbapenems resistance in Gram-negative bacilli isolates in an intensive care unit

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Objective: to determine resistance of *Ps. aeruginosa*, *A. baumannii* and *K. pneumonniae* as prevalent nosocomial agents to commonly used antibiotics including imipenem, meropenem and ertapenem.
Methods: Identification of microorganisms and susceptibility test was performed with the Vitek 2 (BioMerieux®, France) and the susceptibility disc diffusion method according to CLSI directions. For *Klebsiella spp.* extended-spectrum Beta-lactamases (ESBLs) production was confirmed by double-disc test. To screen for metallo-b-lactamase production (MBL), a synergy test using an imipenem and EDTA-containing discs was employed. Quality control was ensured by keeping weekly records of disk diffusion *Ps. aeruginosa* (ATCC 27853). MIC values for carbapenems were determined by the E-test (AB Biodisk, Solona, Sweden) as recommended by manufacture. *K. pneumoniae* ATCC 70603 was used as a positive ESBLs strain.
Results: Information was available on antibiotic suceptibility of 1044 gram-negative bacteria, of which the most common were *A. baumanii* 414, *Ps. aeruginosa* 328, *K. pneumoniae* 169. No duplicate isolates from the same patients were included. All microorganisms were isolated from tracheal tube aspirates, urine, wound, blood and other sterile body fluids. The resistance rates (%) of *A. baumanii, Ps. aeruginosa*, and *K. pneumoniae* were: imipenem 76/61/67, meropenem 68/52/65, ertapenem 77/65/68, amikacin 88/48/40, piperacillin/tazobactam 82/35/67, ceftazidime 100/68/65, ciprofloxacin 92/64/15, aztreonam 100/84/72. Of 169 isolates of *K. pneumoniae* 92 (54,43%) were ESBls.
Conclusions: The most isolates of *A. baumannii* were multi-drug resistant. The majority of isolates were resistant to 5 or more antibiotics tested and some strains were defined by resistance to all antimicrobial agents except colistin. The resistance to carbapenems rose dramatically.

OL-008 Molecular characterization of extended-spectrum β-lactamases and AmpC enzymes in Enterobacteriaceae in Beijing, China

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Objectives: A study was conducted to evaluate the molecular characterization of extended-spectrum β-lactamases (ESBLs) and plasmid-mediated AmpC enzymes in *Enterobacteriaceae* in Beijing, China.
Methods: Production of ESBLs and plasmid-mediated AmpC among 240 non-duplicate *Enterobacteriaceae* isolates was screened by the phenotypic methods and the molecular methods. The epidemiological relationship of the isolates was studied by random amplified polymorphic DNA (RAPD) analysis.
Results: CTX-M type ESBLs were the most prevalent ESBLs. Three *E. coli* isolates simultaneously harbored $bla_{CTX\text{-}M\text{-}3}$ and $bla_{CTX\text{-}M\text{-}9}$ genes. SHV-12 was the most prevalent SHV-type ESBL. SHV-2a, SHV-2 and SHV-5 ESBLs, and SHV-27 and SHV-44 non-ESBLs were detected. Two *Klebsiella pneumoniae* isolates expressed a novel ESBL, SHV-43a, which had one substitution (Leu35Gln) compared with SHV-43. DHA-1 was the most prevalent plasmid-mediated AmpC enzyme, found mainly in *K. pneumoniae* (n=11). We also identified the plasmid-mediated CMY-2 enzyme in two *E. coli* isolates. RAPD analysis revealed that 53 CTX-M-13- and 7 CTX-M-3-producing *E. cloacae* isolates recovered from a single hospital exhibited a high similarity of RAPD patterns, indicating clone-related spread.
Conclusions: This survey indicates the high frequencies of CTX-M-9/3 ESBLs and plasmid-mediated DHA-1 in China, reports the first emergence of DHA-1-producing *E. cloacae* and interhospital epidemic CTX-M-13/3-producing *E. cloacae*.

OL-009 Virulence factors determination and molecular characterisation of Malaysian *Vibrio cholerae*

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Objective: To determine the virulence profiles of Malaysian *Vibrio cholerae* and to investigate the relatedness of the strains using molecular typing methods.
Methods: 43 *V. cholerae* were isolated from clinical and environmental sources. Strains isolated were serogrouped and PCR were carried out for determination of the virulence genes harbored in each strain. The strains were further characterized using molecular subtyping methods such as RAPD, ERIC, REP-PCR and PFGE fingerprinting to investigate the relatedness among the strains.
Results: Twenty-three O1, one O139 and 19 non-O1/nonO139 strains were isolated. All but one O1 strains harbored virulence genes such as *ctx*A, *zot*, *rtx*A, *rst*R, toxT, *tox*R, *tcp*A, *tcp*I, and